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16

## RAW SEQUENCE LISTING

DATE: 11/13/2003

PATENT APPLICATION: US/09/862,802A

TIME: 15:55:57

Input Set : A:\SF0695BUS.ST25.txt

Output Set: N:\CRF4\11132003\I862802A.raw

3 <110> APPLICANT: Valladeau, Jenny  
4 Ravel, Odile  
5 Bates, Elizabeth Ester Mary  
6 Ford, John  
7 Lebecque, Serge J.E.  
8 Saeland, Sem  
10 <120> TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents  
12 <130> FILE REFERENCE: SF0695 B  
14 <140> CURRENT APPLICATION NUMBER: US 09/862,802A  
15 <141> CURRENT FILING DATE: 2001-05-22  
17 <150> PRIOR APPLICATION NUMBER: US 60/053,080  
18 <151> PRIOR FILING DATE: 1997-07-09  
20 <150> PRIOR APPLICATION NUMBER: US 09/111,470  
21 <151> PRIOR FILING DATE: 1998-07-08  
23 <160> NUMBER OF SEQ ID NOS: 13  
25 <170> SOFTWARE: PatentIn version 3.1  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 1104  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Unknown  
32 <220> FEATURE:  
33 <223> OTHER INFORMATION: mammalian nucleic acid and protein  
35 <220> FEATURE:  
36 <221> NAME/KEY: CDS  
37 <222> LOCATION: (242)..(952)  
38 <223> OTHER INFORMATION:

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46 ctccactagt tgagtgaag gaaggaggta atttaccacc atgtttggtt cctgtttata      180
48 agatgtttta agaaagattt gaaacagatt ttctgaagaa agcagaagct ctcttcccat      240
50 t atg act tcg gaa atc act tat gct gaa gtg agg ttc aaa aat gaa ttc      289
51 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
52 1          5          10          15
54 aag tcc tca ggc atc aac aca gcc tct tct gca gct tcc aag gag agg      337
55 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
56          20          25          30
58 act gcc cct ctc aaa agt aat acc gga ttc ccc aag ctg ctt tgt gcc      385
59 Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
60          35          40          45
62 tca ctg ttg ata ttt ttc ctg cta ttg gca atc tca ttc ttt att gct      433
63 Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
64          50          55          60

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66 ttt gtc att ttc ttt caa aaa tat tct cag ctt ctt gaa aaa aag act      481
67 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
68 65                               70                               75                               80
70 aca aaa gag ctg gtt cat aca aca ttg gag tgt gtg aaa aaa aat atg      529
71 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
72                               85                               90                               95
74 ccc gtg gaa gag aca gcc tgg agc tgt tgc cca aag aat tgg aag tca      577
75 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
76                               100                              105                              110
78 ttt agt tcc aac tgc tac ttt att tct act gaa tca gca tct tgg caa      625
79 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
80                               115                              120                              125
82 gac agt gag aag gac tgt gct aga atg gag gct cac ctg ctg gtg ata      673
83 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
84                               130                              135                              140
86 aac act caa gaa gag cag gat ttc atc ttc cag aat ctg caa gaa gaa      721
87 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
88 145                               150                              155                              160
90 tct gct tat ttt gtg ggg ctc tca gat cca gaa ggt cag cga cat tgg      769
91 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
92                               165                              170                              175
94 caa tgg gtt gat cag aca cca tac aat gaa agt tcc aca ttc tgg cat      817
95 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
96                               180                              185                              190
98 cca cgt gag ccc agt gat ccc aat gag cgc tgc gtt gtg cta aat ttt      865
99 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
100                               195                              200                              205
102 cgt aaa tca ccc aaa aga tgg ggc tgg aat gat gtt aat tgt ctt ggt      913
103 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
104                               210                              215                              220
106 cct caa agg tca gtt tgt gag atg atg aag atc cac tta tgaactgaac      962
107 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
108 225                               230                              235
110 attctccatg aacaggtggt tggattggta tctgtcattg tagggataga taataagctc 1022
112 ttcttattca tgtgtaaggg aggtccatag aatttaggtg gtctgtcaac tattctactt 1082
114 atgagagaat tggctctgtac at                                           1104
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118 <211> LENGTH: 237
119 <212> TYPE: PRT
120 <213> ORGANISM: Unknown
122 <220> FEATURE:
123 <223> OTHER INFORMATION: mammalian nucleic acid and protein
125 <400> SEQUENCE: 2
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128 1                               5                               10                               15
131 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
132                               20                               25                               30
135 Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
136                               35                               40                               45

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139 Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
140      50      55      60
143 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Glu Lys Lys Thr
144 65      70      75      80
147 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
148      85      90      95
151 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
152      100      105      110
155 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
156      115      120      125
159 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
160      130      135      140
163 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
164 145      150      155      160
167 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
168      165      170      175
171 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
172      180      185      190
175 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
176      195      200      205
179 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
180      210      215      220
183 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
184 225      230      235

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187 &lt;210&gt; SEQ ID NO: 3

188 &lt;211&gt; LENGTH: 1458

189 &lt;212&gt; TYPE: DNA

190 &lt;213&gt; ORGANISM: Unknown

192 &lt;220&gt; FEATURE:

193 &lt;223&gt; OTHER INFORMATION: mammalian nucleic acid and protein

195 &lt;220&gt; FEATURE:

196 &lt;221&gt; NAME/KEY: CDS

197 &lt;222&gt; LOCATION: (257)..(1204)

198 &lt;223&gt; OTHER INFORMATION: protein coding sequence

201 &lt;220&gt; FEATURE:

202 &lt;221&gt; NAME/KEY: misc\_feature

203 &lt;222&gt; LOCATION: (608)..(673)

204 &lt;223&gt; OTHER INFORMATION: short form lacks nucleotides 608-673

207 &lt;220&gt; FEATURE:

208 &lt;221&gt; NAME/KEY: misc\_feature

209 &lt;222&gt; LOCATION: (775)..(776)

210 &lt;223&gt; OTHER INFORMATION: ASGPRm (Table 2) has sequence insert encoding GEE between nucleotides 775-776

214 &lt;220&gt; FEATURE:

215 &lt;221&gt; NAME/KEY: misc\_feature

216 &lt;222&gt; LOCATION: (1064)..(1064)

217 &lt;223&gt; OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather than Asp at the residue numbered 270

221 &lt;400&gt; SEQUENCE: 3

## RAW SEQUENCE LISTING

DATE: 11/13/2003

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TIME: 15:55:57

Input Set : A:\SF0695BUS.ST25.txt

Output Set: N:\CRF4\11132003\I862802A.raw

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222 gttgaggaga tgggatgtcc cagatgatag ggctcctggg atttcagacc caagaccagc      60
224 aggactccag tcacctctac cccagctctc caggacacag cgctcccaac tctgagtgc      120
226 gtcccacctc tggctcttgc agcacaacca acgtgggaat cacacctcc agacctccca      180
228 cagctccacc ccagactggg cgccggccct gcctccattt cagctgtgac aacctcagag      240
230 ccgtgttggc ccaagc atg aca agg acg tat gaa aac ttc cag tac ttg gag      292
231                               Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu
232                               1           5           10
234 aat aag gtg aaa gtc cag ggg ttt aaa aat ggg cca ctt cct ctc cag      340
235 Asn Lys Val Lys Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln
236           15           20           25
238 tcc ctc ctg cag cgt ctc cgc tct ggg ccc tgc cat ctc ctg ctg tcc      388
239 Ser Leu Leu Gln Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser
240           30           35           40
242 ctg ggc ctc ggc ctg ctg ctg ctg gtc atc atc tgt gtg gtt gga ttc      436
243 Leu Gly Leu Gly Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe
244 45           50           55           60
246 caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca gat ttt      484
247 Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe
248           65           70           75
250 agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg act tcc      532
251 Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser
252           80           85           90
254 cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct gag gtg      580
255 Gln Gly Ser Ser Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val
256           95           100           105
258 gag ggt ttc aag cag gaa cgg cag gca ggg gta tct gag ctc cag gaa      628
259 Glu Gly Phe Lys Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu
260           110           115           120
262 cac act acg cag aag gca cac cta ggc cac tgt ccc cac tgc cca tct      676
263 His Thr Thr Gln Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser
264 125           130           135           140
266 gtg tgt gtc cca gtt cat tct gaa atg ctc ctg cga gtc cag cag ctg      724
267 Val Cys Val Pro Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu
268           145           150           155
270 gtg caa gac ctg aag aaa ctg acc tgc cag gtg gct act ctc aac aac      772
271 Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn
272           160           165           170
274 aat gcc tcc act gaa ggg acc tgc tgc ccc gtc aac tgg gtg gag cac      820
275 Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His
276           175           180           185
278 caa gac agc tgc tac tgg ttc tct cac tct ggg atg tcc tgg gcc gag      868
279 Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu
280           190           195           200
282 gct gag aag tac tgc cag ctg aag aac gcc cac ctg gtg gtc atc aac      916
283 Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn
284 205           210           215           220
286 tcc agg gag gag cag aat ttt gtc cag aaa tat cta ggc tcc gca tac      964
287 Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr
288           225           230           235

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Input Set : A:\SF0695BUS.ST25.txt

Output Set: N:\CRF4\11132003\I862802A.raw

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290 acc tgg atg ggc ctc agt gac cct gaa gga gcc tgg aag tgg gtg gat      1012
291 Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp
292          240          245          250
294 gga aca gac tat gcg acc ggc ttc cag aac tgg aag cca ggc cag cca      1060
295 Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro
296          255          260          265
298 gac gac tgg cag ggg cac ggg ctg ggt gga ggc gag gac tgt gct cac      1108
299 Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala His
300          270          275          280
302 ttc cat cca gac ggc agg tgg aat gac gac gtc tgc cag agg ccc tac      1156
303 Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr
304 285          290          295          300
306 cac tgg gtc tgc gag gct ggc ctg ggt cag acc agc cag gag agt cac      1204
307 His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
308          305          310          315
310 tgagctgcct ttggtgggac caccgggcca cagaaatggc ggtgggagga ggactcttct      1264
312 cagcactcc tcgcaagacc gctctgggag agaaataagc actgggagat tggaagcact      1324
314 gctaacattt tgaatttttt tctctttaat tttaaaaaga tggatatagtg ttcttaagct      1384
316 tttatttttt ttccaacttt tgaaagtcaa cttcatgaag gtataatttt tacataataa      1444
318 aaatgcactc attt      1458
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322 <211> LENGTH: 316
323 <212> TYPE: PRT
324 <213> ORGANISM: Unknown
326 <220> FEATURE:
327 <223> OTHER INFORMATION: mammalian nucleic acid and protein
329 <220> FEATURE:
330 <221> NAME/KEY: misc_feature
331 <222> LOCATION: (608)..(673)
332 <223> OTHER INFORMATION: short form lacks nucleotides 608-673
334 <220> FEATURE:
335 <221> NAME/KEY: misc_feature
336 <222> LOCATION: (775)..(776)
337 <223> OTHER INFORMATION: ASGPRm (Table 2) has sequence insert encoding GEE between nucleot
338      ides 775-776
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (1064)..(1064)
343 <223> OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
344      than Asp at the residue numbered 270
346 <400> SEQUENCE: 4
348 Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
349 1          5          10          15
352 Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
353          20          25          30
356 Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
357          35          40          45
360 Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
361          50          55          60

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## VERIFICATION SUMMARY

DATE: 11/13/2003

PATENT APPLICATION: US/09/862,802A

TIME: 15:55:58

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Output Set: N:\CRF4\11132003\I862802A.raw

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